

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Gary S. Gray et al.
- (ii) TITLE OF INVENTION: CTLA-4-C γ 4 Fusion Proteins (As Amended)
- (iii) NUMBER OF SEQUENCES: 32
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: LAHIVE & COCKFIELD
 - (B) STREET: 28 State Street
 - (C) CITY: Boston
 - (D) STATE: Massachusetts
 - (E) COUNTRY: USA
 - (F) ZIP: 02109-1875
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: Not yet available
 - (B) FILING DATE: December 20, 2001
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 09/227,595
 - (B) FILING DATE: January 8, 1999
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Amy E. Mandragouras
 - (B) REGISTRATION NUMBER: 36,207
 - (C) REFERENCE/DOCKET NUMBER: RPN-001CN
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (617)227-7400
 - (B) TELEFAX: (617)227-5941

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CATTCTAGAA CCTCGACAAG CTTGAGATCA CAGTTCTCTC TAC

43

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CAGCAGGCTG GGCCACGTGC ATTGCGGAGT GGACACCTGT GGAGAG

46

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTCTCCACAG GTGTCCACTC CGCAATGCAC GTGGCCCAGC CTGCTG

46

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TGTGTGTGGA ATTCTCATTA CTGATCAGAA TCTGGGCACG GTTCTG

46

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 78 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GCATTTTAAG CTTTTTCCTG ATCAGGAGCC CAAATCTTCT GACAAAAC TC ACACATCTCC 60
ACCGTCTCCA GGTAAGCC 78

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TAATACGACT CACTATAGGG 20

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GAGCATTTTC CTGATCAGGA GTCCAAATAT GGTCCCCC AC CCCATCATCC CCAGGTAAGC 60
CAACCC 66

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 68 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GCAGAGGAAT TCGAGCTCGG TACCCGGGGA TCCCCAGTGT GGGGACAGTG GGACCCGCTC 60
TGCCTCCC 68

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGGTTTGGG GGGAAGAGGA AGACTGACGG TGCCCCCTCG GCTTCAGGTG CTGAGGAAG 59

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CATCTCTTCC TCAGCACCTG AAGCCGAGGG GGCACCGTCA GTCTTCCTCT TCCCCC 56

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 99 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CGCACGTGAC CTCAGGGGTC CGGGAGATCA TGAGAGTGTC CTTGGGTTTT GGGGGGAACA 60

GGAAGACTGA TGGTGCCCCC TCGAACTCAG GTGCTGAGG 99

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 99 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CCTCAGCACC TGAGTTCGAG GGGGCACCAT CAGTCTTCCT GTTCCCCCA AAACCCAAGG 60
ACACTCTCAT GATCTCCCGG ACCCCTGAGG TCACGTGCG 99

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CATTGCTTA CCTCGACAAG CTTGAGATCA CAGTTCTCTC TAC 43

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GGAGTGGACA CCTGTGGAGA G 21

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CTCCACAGGT GTCCACTCCG CAATGCACGT GGCCCAGCC

39

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GAGGTTGTAA GGA CTCACCT GAAATCTGGG CTC CGTTGC

39

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GCAACGGAGC CCAGATTTCA GGTGAGTCCT TACAACCTC

39

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GGCTAGATAT CTCTAGACTA TAAATCTCTG GCCATGAAG

39

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

10027075-12001

(ii) MOLECULE TYPE: cDNA

GGCACTAGGT CGACTCTAGA AACTGAGGAA GCAAAGTTTA AATTCTACTC ACGTTTAAATC 60

TGGGCTCCGT TGC 73

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GCAGAGAGAG GATCCTCAGT CAGTTAGTCA GAATCTGGGC ACGGTTCTGG 50

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 107 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GGCACTAGTC ATGAAATACC TATTGCCTAC GGCAGCCGCT GGATTGTTAT TACTCGCTGC	60
CCAACCAGCG ATGGCCGCAG CAATGCACGT GGCCAGCCT GCTGTGG	107

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1705 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CATTGCTTA CCTCGAGAAG CTTGAGATCA CAGTTCTCTC TACAGTTACT GAGCACACAG	60
GACCTCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG TAGCAACAGC TACAGGTAAG	120
GGGCTCACAG TAGCAGGCTT GAGGTCTGGA CATATATATG GGTGACAATG ACATCCACTT	180
TGCCTTTCTC TCCACAGGTG TCCACTCCGC AATGCACGTG GCCCAGCCTG CTGTGGTACT	240
GGCCAGCAGC CGAGGCATCG CCAGCTTTGT GTGTGAGTAT GCATCTCCAG GCAAAGCCAC	300
TGAGGTCCGG GTGACAGTGC TTCGGCAGGC TGACAGCCAG GTGACTGAAG TCTGTGCGGC	360
AACCTACATG ATGGGGAATG AGTTGACCTT CCTAGATGAT TCCATCTGCA CGGGCACCTC	420
CAGTGGAAT CAAGTGAACC TCACTATCCA AGGACTGAGG GCCATGGACA CGGGACTCTA	480
CATCTGCAAG GTGGAGCTCA TGTACCCACC GCCATACTAC CTGGGCATAG GCAACGGAAC	540
CCAGATTTAT GTAATTGATC CAGAACCGTG CCCAGATTCT GATCAGGAGC CCAAATCTTC	600
TGACAAAAC CACACATCTC CACCGTCTCC AGGTAAGCCA GCCCAGGCCT CGCCCTCCAG	660
CTCAAGGCGG GACAGGTGCC CTAGAGTAGC CTGCATCCAG GGACAGGCCC CAGCCGGGTG	720
CTGACACGTC CACCTCCATC TCTTCCTCAG CACCTGAAGC CGAGGGGGCA CCGTCAGTCT	780
TCCTCTTCCC CCCAAAACCC AAGGACACCC TCATGATCTC CCGGACCCCT GAGGTCACAT	840
GCGTGGTGGT GGACGTGAGC CACGAAGACC CTGAGGTCAA GTTCAACTGG TACGTGGACG	900
GCGTGGAGGT GCATAATGCC AAGACAAAGC CGCGGGAGGA GCAGTACAAC AGCACGTACC	960
GGGTGGTCAG CGTCCTCACC GTCCTGCACC AGGACTGGCT GAATGGCAAG GAGTACAAGT	1020

GCAAGGTCTC CAACAAAGCC CTCCCAGCCC CCATCGAGAA AACCATCTCC AAAGCCAAAG 1080
 GTGGGACCCG TGGGGTGC GA GGGCCACATG GACAGAGGCC GGCTCGGCCC ACCCTCTGCC 1140
 CTGAGAGTGA CCGCTGTACC AACCTCTGTC CTACAGGGCA GCCCCGAGAA CCACAGGTGT 1200
 ACACCCTGCC CCCATCCCGG GATGAGCTGA CCAAGAACCA GGTGAGCCTG ACCTGCCTGG 1260
 TCAAAGGCTT CTATCCCAGC GACATCGCCG TGGAGTGGGA GAGCAATGGG CAGCCGGAGA 1320
 ACAACTACAA GACCACGCCT CCCGTGCTGG ACTCCGACGG CTCCTTCTTC CTCTACAGCA 1380
 AGCTCACCGT GGACAAGAGC AGGTGGCAGC AGGGGAACGT CTTCTCATGC TCCGTGATGC 1440
 ATGAGGCTCT GCACAACCAC TACACGCAGA AGAGCCTCTC CCTGTCTCCG GGTAAATGAG 1500
 TGCACGCGCC GGCAAGCCCC GCTCCCCGGG CTCTCGCGGT CGCACGAGGA TGCTTGGCAC 1560
 GTACCCCCTG TACATACTTC CCGGGCGCCC AGCATGGAAA TAAAGCACCC AGCGCTGCCC 1620
 TGGGCCCCTG CGAGACTGTG ATGGTTCTTT CCACGGGTCA GGCCGAGTCT GAGGCCTGAG 1680
 TGGCATGAGG GAGGCAGAGC GGGTC 1705

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Met	Gly	Tfp	Ser	Cys	Ile	Ile	Leu	Phe	Leu	Val	Ala	Thr	Ala	Thr	Gly
1				5					10					15	
Val	His	Ser	Ala	Met	His	Val	Ala	Gln	Pro	Ala	Val	Val	Leu	Ala	Ser
			20					25					30		
Ser	Arg	Gly	Ile	Ala	Ser	Phe	Val	Cys	Glu	Tyr	Ala	Ser	Pro	Gly	Lys
		35					40					45			
Ala	Thr	Glu	Val	Arg	Val	Thr	Val	Leu	Arg	Gln	Ala	Asp	Ser	Gln	Val
		50				55					60				
Thr	Glu	Val	Cys	Ala	Ala	Thr	Tyr	Met	Met	Gly	Asn	Glu	Leu	Thr	Phe
65					70					75				80	
Leu	Asp	Asp	Ser	Ile	Cys	Thr	Gly	Thr	Ser	Ser	Gly	Asn	Gln	Val	Asn
				85					90					95	

Leu Thr Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys
100 105 110

Lys Val Glu Leu Met Tyr Pro Pro Tyr Tyr Leu Gly Ile Gly Asn
115 120 125

Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
130 135 140

Gln Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro Ser Pro
145 150 155 160

Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys
165 170 175

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
180 185 190

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
195 200 205

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
210 215 220

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
225 230 235 240

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
245 250 255

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
260 265 270

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
275 280 285

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
290 295 300

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
305 310 315 320

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
325 330 335

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
340 345 350

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
355 360 365

Lys Ser Leu Ser Leu Ser Pro Gly Lys
370 375

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1747 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CATTGCTTA	CCTCGAGAAG	CTTGAGATCA	CAGTTCTCTC	TACAGTTACT	GAGCACACAG	60
GACCTCACCA	TGGGATGGAG	CTGTATCATC	CTCTTCTTGG	TAGCAACAGC	TACAGGTAAG	120
GGGCTCACAG	TAGCAGGCTT	GAGGTCTGGA	CATATATATG	GGTGACAATG	ACATCCACTT	180
TGCCTTTCTC	TCCACAGGTG	TCCACTCCGC	AATGCACGTG	GCCCAGCCTG	CTGTGGTACT	240
GGCCAGCAGC	CGAGGCATCG	CCAGCTTTGT	GTGTGAGTAT	GCATCTCCAG	GCAAAGCCAC	300
TGAGGTCCGG	GTGACAGTGC	TTCGGCAGGC	TGACAGCCAG	GTGACTGAAG	TCTGTGCGGC	360
AACCTACATG	ATGGGGAATG	AGTTGACCTT	CCTAGATGAT	TCCATCTGCA	CGGGCACCTC	420
CAGTGAAAT	CAAGTGAACC	TCACTATCCA	AGGACTGAGG	GCCATGGACA	CGGGACTCTA	480
CATCTGCAAG	GTGGAGCTCA	TGTACCCACC	GCCATACTAC	CTGGGCATAG	GCAACGGAAC	540
CCAGATTTAT	GTAATTGATC	CAGAACCGTG	CCCAGATTCT	GATCAGGAGT	CCAAATATGG	600
TCCCCCATCC	CCATCATCCC	CAGGTAAGCC	AACCCAGGCC	TCGCCCTCCA	GCTCAAGGCG	660
GGACAGGTGC	CCTAGAGTAG	CCTGCATCCA	GGGACAGGCC	CCAGCCGGGT	GCTGACGCAT	720
CCACCTCCAT	CTCTTCCTCA	GCACCTGAGT	TCCTGGGGGG	ACCATCAGTC	TTCCTGTTCC	780
CCCCAAAACC	CAAGGACACT	CTCATGATCT	CCCGGACCCC	TGAGGTCACG	TGCGTGGTGG	840
TGGACGTGAG	CCAGGAAGAC	CCCGAGGTCC	AGTTCAACTG	GTACGTGGAT	GGCGTGGAGG	900
TGCATAATGC	CAAGACAAAG	CCGCGGGAGG	AGCAGTTCAA	CAGCACGTAC	CGTGTGGTCA	960
GCGTCCTCAC	CGTCCTGCAC	CAGGACTGGC	TGAACGGCAA	GGAGTACAAG	TGCAAGGTCT	1020
CCAACAAAGG	CCTCCCGTCC	TCCATCGAGA	AAACCATCTC	CAAAGCCAAA	GGTGGGACCC	1080
ACGGGGTGCG	AGGGCCACAC	GGACAGAGGC	CAGCTCGGCC	CACCCTCTGC	CCTGGGAGTG	1140
ACCGCTGTGC	CAACCTCTGT	CCCTACAGGG	CAGCCCCGAG	AGCCACAGGT	GTACACCCTG	1200
CCCCCATCCC	AGGAGGAGAT	GACCAAGAAC	CAGGTCAGCC	TGACCTGCCT	GGTCAAAGGC	1260
TTCTACCCCA	GCGACATCGC	CGTGGAGTGG	GAGAGCAATG	GGCAGCCGGA	GAACAACCTAC	1320
AAGACCACGC	CTCCCGTGCT	GGACTCCGAC	GGCTCCTTCT	TCCTCTACAG	CAGGCTAACC	1380
GTGGACAAGA	GCAGGTGGCA	GGAGGGGAAT	GTCTTCTCAT	GCTCCGTGAT	GCATGAGGCT	1440

CTGCACAACC ACTACACACA GAAGAGCCTC TCCCTGTCTC TGGGTAAATG AGTGCCAGGG 1500
 CCGGCAAGCC CCCGCTCCCC GGGCTCTCGG GGTGCGCGGA GGATGCTTGG CACGTACCCC 1560
 GTCTACATAC TTCCCAGGCA CCCAGCATGG AAATAAAGCA CCCACCACTG CCCTGGGCCC 1620
 CTGTGAGACT GTGATGGTTC TTTCCACGGG TCAGGCCGAG TCTGAGGCCT GAGTGACATG 1680
 AGGGAGGCAG AGCGGTCCCA CTGTCCCCAC ACTGGGGATC CCCGGGTACC GAGCTCGATT 1740
 CCTCTGC 1747

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Met	Gly	Trp	Ser	Cys	Ile	Ile	Leu	Phe	Leu	Val	Ala	Thr	Ala	Thr	Gly	1	5	10	15
Val	His	Ser	Ala	Met	His	Val	Ala	Gln	Pro	Ala	Val	Val	Leu	Ala	Ser	20	25	30	
Ser	Arg	Gly	Ile	Ala	Ser	Phe	Val	Cys	Glu	Tyr	Ala	Ser	Pro	Gly	Lys	35	40	45	
Ala	Thr	Glu	Val	Arg	Val	Thr	Val	Leu	Arg	Gln	Ala	Asp	Ser	Gln	Val	50	55	60	
Thr	Glu	Val	Cys	Ala	Ala	Thr	Tyr	Met	Met	Gly	Asn	Glu	Leu	Thr	Phe	65	70	75	80
Leu	Asp	Asp	Ser	Ile	Cys	Thr	Gly	Thr	Ser	Ser	Gly	Asn	Gln	Val	Asn	85	90	95	
Leu	Thr	Ile	Gln	Gly	Leu	Arg	Ala	Met	Asp	Thr	Gly	Leu	Tyr	Ile	Cys	100	105	110	
Lys	Val	Glu	Leu	Met	Tyr	Pro	Pro	Pro	Tyr	Tyr	Leu	Gly	Ile	Gly	Asn	115	120	125	
Gly	Thr	Gln	Ile	Tyr	Val	Ile	Asp	Pro	Glu	Pro	Cys	Pro	Asp	Ser	Asp	130	135	140	
Gln	Glu	Ser	Lys	Tyr	Gly	Pro	Pro	Ser	Pro	Ser	Ser	Pro	Ala	Pro	Glu	145	150	155	160
Phe	Glu	Gly	Ala	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	165	170	175	

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
180 185 190

Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly
195 200 205

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn
210 215 220

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
225 230 235 240

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro
245 250 255

Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
260 265 270

Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn
275 280 285

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
290 295 300

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
305 310 315 320

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg
325 330 335

Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys
340 345 350

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
355 360 365

Ser Leu Ser Leu Gly Lys
370

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1747 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CATTCGCTTA	CCTCGAGAAG	CTTGAGATCA	CAGTTCCTCTC	TACAGTTACT	GAGCACACAG	60
GACCTCACCA	TGGGATGGAG	CTGTATCATC	CTCTTCTTGG	TAGCAACAGC	TACAGGTAAG	120
GGGCTCACAG	TAGCAGGCTT	GAGGTCTGGA	CATATATATG	GGTGACAATG	ACATCCACTT	180
TGCCTTTCTC	TCCACAGGTG	TCCACTCCGC	AATGCACGTG	GCCCAGCCTG	CTGTGGTACT	240
GGCCAGCAGC	CGAGGCATCG	CCAGCTTTGT	GTGTGAGTAT	GCATCTCCAG	GCAAAGCCAC	300
TGAGGTCCGG	GTGACAGTGC	TTCGGCAGGC	TGACAGCCAG	GTGACTGAAG	TCTGTGCGGC	360
AACCTACATG	ATGGGGAATG	AGTTGACCTT	CCTAGATGAT	TCCATCTGCA	CGGGCACCTC	420
CAGTGAAAT	CAAGTGAACC	TCACTATCCA	AGGACTGAGG	GCCATGGACA	CGGGACTCTA	480
CATCTGCAAG	GTGGAGCTCA	TGTACCCACC	GCCATACTAC	CTGGGCATAG	GCAACGGAAC	540
CCAGATTTAT	GTAATTGATC	CAGAACCGTG	CCCAGATTCT	GATCAGGAGT	CCAAATATGG	600
TCCCCATCC	CCATCATCCC	CAGGTAAGCC	AACCCAGGCC	TCGCCCTCCA	GCTCAAGGCG	660
GGACAGGTGC	CCTAGAGTAG	CCTGCATCCA	GGGACAGGCC	CCAGCCGGGT	GCTGACGCAT	720
CCACCTCCAT	CTCTTCCTCA	GCACCTGAGT	TCGAGGGGGC	ACCATCAGTC	TTCCTGTTCC	780
CCCCAAAACC	CAAGGACACT	CTCATGATCT	CCCGGACCCC	TGAGGTCACG	TGCGTGGTGG	840
TGGACGTGAG	CCAGGAAGAC	CCCGAGGTCC	AGTTCAACTG	GTACGTGGAT	GGCGTGGAGG	900
TGCATAATGC	CAAGACAAAG	CCGCGGGAGG	AGCAGTTCAA	CAGCACGTAC	CGTGTGGTCA	960
GCGTCCTCAC	CGTCCTGCAC	CAGGACTGGC	TGAACGGCAA	GGAGTACAAG	TGCAAGGTCT	1020
CCAACAAAGG	CCTCCCGTCC	TCCATCGAGA	AAACCATCTC	CAAAGCCAAA	GGTGGGACCC	1080
ACGGGGTGCG	AGGGCCACAC	GGACAGAGGC	CAGCTCGGCC	CACCCCTCTGC	CCTGGGAGTG	1140
ACCGCTGTGC	CAACCTCTGT	CCCTACAGGG	CAGCCCCGAG	AGCCACAGGT	GTACACCCTG	1200
CCCCCATCCC	AGGAGGAGAT	GACCAAGAAC	CAGGTCAGCC	TGACCTGCCT	GGTCAAAGGC	1260
TTCTACCCCA	GCGACATCGC	CGTGGAGTGG	GAGAGCAATG	GGCAGCCGGA	GAACAACTAC	1320
AAGACCACGC	CTCCCGTGCT	GGACTCCGAC	GGCTCCTTCT	TCCTCTACAG	CAGGCTAACC	1380
GTGGACAAGA	GCAGGTGGCA	GGAGGGGAAT	GTCTTCTCAT	GCTCCGTGAT	GCATGAGGCT	1440
CTGCACAACC	ACTACACACA	GAAGAGCCTC	TCCCTGTCTC	TGGGTAAATG	AGTGCCAGGG	1500
CCGGCAAGCC	CCCGCTCCCC	GGGCTCTCGG	GGTCGCGCGA	GGATGCTTGG	CACGTACCCC	1560
GTCTACATAC	TTCCCAGGCA	CCCAGCATGG	AAATAAAGCA	CCCACCACTG	CCCTGGGCCC	1620
CTGTGAGACT	GTGATGGTTC	TTTCCACGGG	TCAGGCCGAG	TCTGAGGCCT	GAGTGACATG	1680
AGGGAGGCGAG	AGCGGTCCCA	CTGTCCCCAC	ACTGGGGATC	CCCGGGTACC	GAGCTCGATT	1740

CCTCTGC

1747

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Met	Gly	Trp	Ser	Cys	Ile	Ile	Leu	Phe	Leu	Val	Ala	Thr	Ala	Thr	Gly	1	5	10	15
Val	His	Ser	Ala	Met	His	Val	Ala	Gln	Pro	Ala	Val	Val	Leu	Ala	Ser	20	25	30	
Ser	Arg	Gly	Ile	Ala	Ser	Phe	Val	Cys	Glu	Tyr	Ala	Ser	Pro	Gly	Lys	35	40	45	
Ala	Thr	Glu	Val	Arg	Val	Thr	Val	Leu	Arg	Gln	Ala	Asp	Ser	Gln	Val	50	55	60	
Thr	Glu	Val	Cys	Ala	Ala	Thr	Tyr	Met	Met	Gly	Asn	Glu	Leu	Thr	Phe	65	70	75	80
Leu	Asp	Asp	Ser	Ile	Cys	Thr	Gly	Thr	Ser	Ser	Gly	Asn	Gln	Val	Asn	85	90	95	
Leu	Thr	Ile	Gln	Gly	Leu	Arg	Ala	Met	Asp	Thr	Gly	Leu	Tyr	Ile	Cys	100	105	110	
Lys	Val	Glu	Leu	Met	Tyr	Pro	Pro	Pro	Tyr	Tyr	Leu	Gly	Ile	Gly	Asn	115	120	125	
Gly	Thr	Gln	Ile	Tyr	Val	Ile	Asp	Pro	Glu	Pro	Cys	Pro	Asp	Ser	Asp	130	135	140	
Gln	Glu	Ser	Lys	Tyr	Gly	Pro	Pro	Ser	Pro	Ser	Ser	Pro	Ala	Pro	Glu	145	150	155	160
Phe	Glu	Gly	Ala	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	165	170	175	
Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	180	185	190	
Val	Ser	Gln	Glu	Asp	Pro	Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	195	200	205	

Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	
210						215					220					
Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	
225				230						235					240	
Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	
			245						250					255		
Ser	Ser	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	
		260						265					270			
Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Gln	Glu	Glu	Met	Thr	Lys	Asn	
	275					280						285				
Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	
	290					295					300					
Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	
305					310					315					320	
Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Arg	
			325						330					335		
Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser	Cys	
		340						345					350			
Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	
	355						360					365				
Ser	Leu	Ser	Leu	Gly	Lys											
	370															

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2770 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CATTCGCTTA CCTCGAGAAG CTTGAGATCA CAGTTCTCTC TACAGTTACT GAGCACACAG	60
GACCTCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG TAGCAACAGC TACAGGTAAG	120
GGGCTCACAG TAGCAGGCTT GAGGTCTGGA CATATATATG GGTGACAATG ACATCCACTT	180
TGCCTTTCTC TCCACAGGTG TCCACTCCGC AATGCACGTG GCCCAGCCTG CTGTGGTACT	240
GGCCAGCAGC CGAGGCATCG CCAGCTTTGT GTGTGAGTAT GCATCTCCAG GCAAAGCCAC	300

TGAGGTCCGG	GTGACAGTGC	TTCGGCAGGC	TGACAGCCAG	GTGACTGAAG	TCTGTGCGGC	360
AACCTACATG	ATGGGGAATG	AGTTGACCTT	CCTAGATGAT	TCCATCTGCA	CGGGCACCTC	420
CAGTGGAAT	CAAGTGAACC	TCACTATCCA	AGGACTGAGG	GCCATGGACA	CGGGACTCTA	480
CATCTGCAAG	GTGGAGCTCA	TGTACCCACC	GCCATACTAC	CTGGGCATAG	GCAACGGAGC	540
CCAGATTTC	GGTGAGTCCT	TACAACCTCT	CTCTTCTATT	CAGCTTAAAT	AGATTTTACT	600
GCATTTGTTG	GGGGGGAAT	GTGTGTATCT	GAATTTTCAGG	TCATGAAGGA	CTAGGGACAC	660
CTTGGGAGTC	AGAAAGGGTC	ATTGGGAGCC	CGGGCTGATG	CAGACAGACA	TCCTCAGCTC	720
CCAGACTTCA	TGGCCAGAGA	TTTATAGTCT	AGAGGATCCC	CAGCTTTCTG	GGGCAGGCCA	780
GGCCTGACCT	TGGCTTTGGG	GCAGGGAGGG	GGCTAAGGTG	AGGCAGGTGG	CGCCAGCAGG	840
TGCACACCCA	ATGCCCATGA	GCCCAGACAC	TGGACGCTGA	ACCTCGCGGA	CAGTTAAGAA	900
CCCAGGGGCC	TCTGCGCCTG	GGCCCAGCTC	TGTCCACAC	CGCGGTCACA	TGGCACCACC	960
TCTCTTGAG	CCTCCACCAA	GGGCCCATCG	GTCTTCCCC	TGGCACCTC	CTCCAAGAGC	1020
ACCTCTGGGG	GCACAGCGGC	CCTGGGCTGC	CTGGTCAAGG	ACTACTTCCC	CGAACCGGTG	1080
ACGGTGTCGT	GGAATCAGG	CGCCCTGACC	AGCGGCGTGC	ACACCTTCCC	GGCTGTCCTA	1140
CAGTCCTCAG	GACTCTACTC	CCTCAGCAGC	GTGGTGACCG	TGCCCTCCAG	CAGCTTGGGC	1200
ACCCAGACCT	ACATCTGCAA	CGTGAATCAC	AAGCCCAGCA	ACACCAAGGT	GGACAAGAAA	1260
GTTGGTGAGA	GGCCAGCACA	GGGAGGGAGG	GTGTCTGCTG	GAAGCAGGCT	CAGCGCTCCT	1320
GCCTGGACGC	ATCCCGGCTA	TGCAGCCCCA	GTCCAGGGCA	GCAAGGCAGG	CCCCGTCTGC	1380
CTCTTCACCC	GGAGCCTCTG	CCCGCCCCAC	TCATGCTCAG	GGAGAGGGTC	TTCTGGCTTT	1440
TTCCCAGGCT	CTGGGCAGGC	ACAGGCTAGG	TGCCCCTAAC	CCAGGCCCTG	CACACAAAGG	1500
GGCAGGTGCT	GGGCTCAGAC	CTGCCAAGAG	CCATATCCGG	GAGGACCCTG	CCCCTGACCT	1560
AAGCCCACCC	CAAAGGCCAA	ACTCTCCACT	CCCTCAGCTC	GGACACCTTC	TCTCCTCCCA	1620
GATTCCAGTA	ACTCCCAATC	TTCTCTCTGC	AGAGCCCAAA	TCTTGTGACA	AAACTCACAC	1680
ATGCCACCG	TGCCCAGGTA	AGCCAGCCCA	GGCCTCGCCC	TCCAGCTCAA	GGCGGGACAG	1740
GTGCCCTAGA	GTAGCCTGCA	TCCAGGGACA	GGCCCCAGCC	GGGTGCTGAC	ACGTCCACCT	1800
CCATCTCTTC	CTCAGCACCT	GAACCTCTGG	GGGGACCGTC	AGTCTTCCTC	TTCCCCCAA	1860
AACCCAAGGA	CACCCTCATG	ATCTCCCGGA	CCCCTGAGGT	CACATGCGTG	GTGGTGACG	1920
TGAGCCACGA	AGACCCTGAG	GTCAAGTTCA	ACTGGTACGT	GGACGGCGTG	GAGGTGCATA	1980
ATGCCAAGAC	AAAGCCGCGG	GAGGAGCAGT	ACAACAGCAC	GTACCGGGTG	GTCAGCGTCC	2040

TCACCGTCCT GCACCAGGAC TGGCTGAATG GCAAGGAGTA CAAGTGCAAG GTCTCCAACA 2100
AAGCCCTCCC AGCCCCCATC GAGAAAACCA TCTCCAAAGC CAAAGGTGGG ACCCGTGGGG 2160
TGCGAGGGCC ACATGGACAG AGGCCGGCTC GGCCACCCCT CTGCCCTGAG AGTGACCGCT 2220
GTACCAACCT CTGTCTTACA GGGCAGCCCC GAGAACCACA GGTGTACACC CTGCCCCCAT 2280
CCCCGGATGA GCTGACCAAG AACCAGGTCA GCCTGACCTG CCTGGTCAAA GGCTTCTATC 2340
CCAGCGACAT CGCCGTGGAG TGGGAGAGCA ATGGGCAGCC GGAGAACAAC TACAAGACCA 2400
CGCCTCCCGT GCTGGACTCC GACGGCTCCT TCTTCTCTA CAGCAAGCTC ACCGTGGACA 2460
AGAGCAGGTG GCAGCAGGGG AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA 2520
ACCACTACAC GCAGAAGAGC CTCTCCCTGT CTCCGGGTAA ATGAGTGCGA CGCCCGGCAA 2580
GCCCCGCTCC CCGGGCTCTC GCGGTCGCAC GAGGATGCTT GGCACGTACC CCCTGTACAT 2640
ACTTCCCGGG CGCCAGCAT GGAAATAAAG CACCCAGCGC TGCCCTGGGC CCCTGCGAGA 2700
CTGTGATGGT TCTTTCCACG GGTCAGGCCG AGTCTGAGGC CTGAGTGGCA TGAGGGAGGC 2760
AGAGCGGGTC 2770

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Met	Gly	Trp	Ser	Cys	Ile	Ile	Leu	Phe	Leu	Val	Ala	Thr	Ala	Thr	Gly
1				5			10							15	
Val	His	Ser	Ala	Met	His	Val	Ala	Gln	Pro	Ala	Val	Val	Leu	Ala	Ser
			20				25						30		
Ser	Arg	Gly	Ile	Ala	Ser	Phe	Val	Cys	Glu	Tyr	Ala	Ser	Pro	Gly	Lys
		35				40					45				
Ala	Thr	Glu	Val	Arg	Val	Thr	Val	Leu	Arg	Gln	Ala	Asp	Ser	Gln	Val
		50				55				60					
Thr	Glu	Val	Cys	Ala	Ala	Thr	Tyr	Met	Met	Gly	Asn	Glu	Leu	Thr	Phe
65				70						75				80	
Leu	Asp	Asp	Ser	Ile	Cys	Thr	Gly	Thr	Ser	Ser	Gly	Asn	Gln	Val	Asn
				85					90					95	

Leu Thr Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys
100 105 110

Lys Val Glu Leu Met Tyr Pro Pro Tyr Tyr Leu Gly Ile Gly Asn
115 120 125

Gly Ala Gln Ile Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro
130 135 140

Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu
145 150 155 160

Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn
165 170 175

Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser
180 185 190

Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala
195 200 205

Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly
210 215 220

Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1708 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CATTCGCTTA CCTCGAGAAG CTTGAGATCA CAGTTCTCTC TACAGTTACT GAGCACACAG	60
GACCTCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG TAGCAACAGC TACAGGTAAG	120
GGGCTCACAG TAGCAGGCTT GAGGTCTGGA CATATATATG GGTGACAATG ACATCCACTT	180
TGCCTTTCTC TCCACAGGTG TCCACTCCGC AATGCACGTG GCCCAGCCTG CTGTGGTACT	240
GGCCAGCAGC CGAGGCATCG CCAGCTTTGT GTGTGAGTAT GCATCTCCAG GCAAAGCCAC	300
TGAGGTCCGG GTGACAGTGC TTCGGCAGGC TGACAGCCAG GTGACTGAAG TCTGTGCGGC	360
AACCTACATG ATGGGGAATG AGTTGACCTT CCTAGATGAT TCCATCTGCA CGGGCACCTC	420
CAGTGGAAT CAAGTGAACC TCACTATCCA AGGACTGAGG GCCATGGACA CGGGACTCTA	480

CATCTGCAAG GTGGAGCTCA TGTACCCACC GCCATACTAC CTGGGCATAG GCAACGGAGC	540
CCAGATTAAA CGTGAGTAGA ATTTAAACTT TGCTTCCTCA GTTTCTAGAA GAATGGCTGC	600
AAAGAGCTCC AACAAAACAA TTTAGAACTT TATTAAGGAA TAGGGGGAAG CTAGGAAGAA	660
ACTCAAAACA TCAAGATTTT AAATACGCTT CTTGGTCTCC TTGCTATAAT TATCTGGGAT	720
AAGCATGCTG TTTTCTGTCT GTCCCTAACA TGCCCTGTGA TTATCCGCAA ACAACACACC	780
CAAGGGCAGA ACTTTGTTAC TTAAACACCA TCCTGTTTGC TTCTTTCCTC AGGAACTGTG	840
GCTGCACCAT CTGTCTTCAT CTTCCCGCCA TCTGATGAGC AGTTGAAATC TGGAAGTGC	900
TCTGTTGTGT GCCTGCTGAA TAACTTCTAT CCCAGAGAGG CCAAAGTACA GTGGAAGGTG	960
GATAACGCCC TCCAATCGGG TAACTCCCAG GAGAGTGTCA CAGAGCAGGA CAGCAAGGAC	1020
AGCACCTACA GCCTCAGCAG CACCCTGACG CTGAGCAAAG CAGACTACGA GAAACACAAA	1080
GTCTACGCCT GCGAAGTCAC CCATCAGGGC CTGAGCTCGC CCGTCACAAA GAGCTTCAAC	1140
AGGGGAGAGT GTTAGAGGGA GAAGTGCCCC CACCTGCTCC TCAGTTCCAG CCTGACCCCC	1200
TCCCATCCTT TGGCCTCTGA CCCTTTTTC ACAGGGGACC TACCCCTATT GCGGTCTCTC	1260
AGCTCATCTT TCACCTCACC CCCCTCCTCC TCCTTGGCTT TAATTATGCT AATGTTGGAG	1320
GAGAATGAAT AAATAAAGTG AATCTTTGCA CCTGTGGTTT CTCTCTTTTC TCAATTTAAT	1380
AATTATTATC TGTGTTTAC CAACTACTCA ATTTCTCTTA TAAGGGACTA AATATGTAGT	1440
CATCCTAAGG CGCATAACCA TTTATAAAAA TCATCCTTCA TTCTATTTTA CCCTATCATC	1500
CTCTGCAAGA CAGTCCTCCC TCAAACCCAC AAGCCTTCTG TCCTCACAGT CCCCTGGGCC	1560
GTGGTAGGAG AGACTTGCTT CCTTGTTTTT CCCTCCTCAG CAAGCCCTCA TAGTCCTTTT	1620
TAAGGGTGAC AGGTCTTACG GTCATATATC CTTTGATTCA ATTCCCTGGG AATCAACCAA	1680
GGCAAATTTT TCAAAAGAAG AAACCTGC	1708

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly

1	5					10					15				
Val	His	Ser	Ala	Met	His	Val	Ala	Gln	Pro	Ala	Val	Val	Leu	Ala	Ser
			20				25						30		
Ser	Arg	Gly	Ile	Ala	Ser	Phe	Val	Cys	Glu	Tyr	Ala	Ser	Pro	Gly	Lys
35						40						45			
Ala	Thr	Glu	Val	Arg	Val	Thr	Val	Leu	Arg	Gln	Ala	Asp	Ser	Gln	Val
50						55						60			
Thr	Glu	Val	Cys	Ala	Ala	Thr	Tyr	Met	Met	Gly	Asn	Glu	Leu	Thr	Phe
65				70						75			80		
Leu	Asp	Asp	Ser	Ile	Cys	Thr	Gly	Thr	Ser	Ser	Gly	Asn	Gln	Val	Asn
			85						90			95			
Leu	Thr	Ile	Gln	Gly	Leu	Arg	Ala	Met	Asp	Thr	Gly	Leu	Tyr	Ile	Cys
			100						105			110			
Lys	Val	Glu	Leu	Met	Tyr	Pro	Pro	Pro	Tyr	Tyr	Leu	Gly	Ile	Gly	Asn
115						120						125			
Gly	Ala	Gln	Ile	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro
130						135						140			
Ser	Asp	Glu	Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu
145				150						155			160		
Asn	Asn	Phe	Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn
			165						170			175			
Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser
			180						185			190			
Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala
195						200						205			
Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	Gly
210						215						220			
Leu	Ser	Ser	Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys		
225				230						235					